

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings of claims in the application:

LISTING OF CLAIMS:

CLAIMS

1-43. (canceled)

44.(new) Mutated V1/AR1/AV1 or C1/AL1/AC1 gene sequence of a tomato infecting geminivirus wherein the mutations consist of point mutations distributed along the sequence in such a way that the continuous homology between the mutated sequence and the corresponding viral gene sequence is below or equal to 8 nucleotides, preferably below or equal to 5 nucleotides, said mutated sequence encoding for a capsid protein or for a Rep protein, respectively.

45.(new) Mutated V1/AR1/AV1 gene sequence according to claim 44, encoding for a capsid protein having sequence SEQ ID No 7.

46.(new) Mutated C1/AL1/AC1 gene sequence according to claim 44, wherein the mutation further comprises a truncation occurring at 3' terminal so that the mutated sequence encodes for a truncated Rep protein.

47.(new) Mutated C1/AL1 /AC1 gene sequences according to claim 46, wherein the truncated Rep proteins consist of 130 aminoacids (Rep 130) to 210 aminoacids (Rep 210).

48.(new) Mutated C1/AL1/AC1 gene sequence according to claim 46 encoding for Rep 210 SEQ ID No 3 or SEQ ID No 5.

49.(new) Mutated C1/AL1/AC1 gene sequence encoding for Rep 130 SEQ ID No 9.

50.(new) Mutated gene sequence according to claim 44 wherein the tomato infecting geminivirus is TYLCSV.

51.(new) Synthetic construct comprising an heterologous polynucleotide sequence containing in the 5'-3' direction:

- a) polynucleotide sequence acting as promoter in said plant or tissue or transformed cells;
- b) a non translated polynucleotide sequence positioned 5' of the encoding region;
- c) a mutated gene sequence;
- d) a sequence acting as transcription terminator, positioned 3' with respect to the mutated gene sequence.

52.(new) Expression vector comprising the construct as defined according to claim 51.

53.(new) Transgenic plant, tissue or plant cells thereof, comprising in their genome a mutated gene sequence according to claim 43.

54.(new) Seed comprising in its genome a mutated gene sequence according to claim 43.

55.(new) Method for the preparation of transgenic plants, plant tissue or cells thereof having long lasting resistance against geminiviruses, including the following steps:

- a) identification or selection of a viral gene sequence encoding an aminoacid sequence able to confer resistance against geminiviruses;

b) mutagenesis of the viral gene sequence so as to make it an ineffective target of the post-transcriptional gene silencing induced by the infecting geminivirus;

c) insertion of the geminivirus gene sequence mutated in the step b) in the plant, plant tissue or cell thereof, using a construct comprising an heterologous polynucleotide sequence containing in the 5'-3' direction:

i) a polynucleotide sequence acting as promoter in said plant or tissue or transformed cells;

ii) a non translated polynucleotide sequence positioned 5' of the encoding region;

iii) a polynucleotide sequence encoding a geminivirus-derived aminoacid sequence, properly mutagenised to be an ineffective target of the post-transcriptional gene silencing induced by the infecting geminivirus;

iv) a sequence acting as transcription terminator positioned 3' with respect to said polynucleotide sequence.

56.(new) Method according to claim 55 wherein the mutations consist of point mutations distributed along the sequence in such a way that the continuous homology between the mutated sequence and the corresponding viral gene sequence is below or equal to 8 nucleotides, preferably below or equal to 5 nucleotides.

57.(new) Method according to claim 55, wherein the mutagenesis in step b) consists of deletions of the 5' or 3' regions of the viral gene sequence of step a) until the identification of the minimum region of said gene sequence that is an ineffective target of the post-transcriptional gene silencing induced by the infecting geminivirus compare to the original viral sequence and that said truncated protein maintains the ability to confer resistance against geminiviruses.

58.(new) Method according to claim 55 wherein the geminiviruses are selected from the group consisting of species of Mastrevirus, Curtovirus, Begomovirus and Topocuvirus and isolates thereof.

59.(new) Method according to claim 58, wherein Begomoviruses species are selected from the group consisting of TYLCCNV, TYLCGV, TYLCMaIV, TYLCSV, TYLCTHV, TYLCV, ACMV, BGMV, CaLCuV, ToCMoV, TGMV, ToGMoV, ToMHV, ToMoTV, ToMoV, ToRMV, ToSLCV, ToSRV, Cotton leaf curl (CLCrV, CLCuAV, C1CuGV, CLCuKV, CLCuMV, CLCuRV), East African cassava mosaic (EACMCV, EACMMV, EACMV, EACMZV), Potato yellow mosaic (PYMPV, PYMTV, PYMV), Squash leaf curl (SLCCNV, SLCV, SLCYV), Sweet potato leaf curl (SPLCGV, SPLCV), Tobacco leaf curl (TbLCJV, TbLCKoV, TbLCYNV, TbLCZV), Tomato leaf curl (ToLCBV, ToLCBDV, ToLCGV, ToLCKV, ToLCLV, ToLCMV, ToLCNDV, ToLCSLV, ToLCTWV, ToLCVV, ToLCV) and isolates thereof.

60.(new) Method according to claim 58, wherein the species belonging to the genus Mastrevirus, Curtovirus, Topocuvirus are selected from the group consisting of WDV, MSV, SSV, BYDV, TYDV, BCTV and isolates thereof.

61.(new) Method according to claim 55, wherein the gene sequence is selected from the group consisting of C1/AL1/AC1, C2/AL2/AC2, C3/AL3/AC3, C4/AL4/AC4, V1/AR1/AV 1, V2/AR2/AV2, BC1/BL1 and BV1/BR1, belonging to the geminiviruses.

62.(new) Method according to claim 61, wherein the C1/AL1/AC1 gene sequence belongs to TYLCSV.

63.(new) Method according to claim 62, wherein the aminoacid sequence is a truncated protein with respect to the viral wild-type protein.

64.(new) Method according to claim 63 wherein the viral gene sequences made ineffective targets of the virus-induced posttranscriptional gene silencing are the SEQ ID No 8, SEQ ID No 2 and SEQ ID No 4.

65.(new) Method according to claim 64, wherein the truncated proteins are Rep-130 (SEQ ID No 9) or Rep-210 (SEQ ID No 3 and 5).

66.(new) Method according to claim 61, wherein the V1/AR1/AV1 gene sequence belongs to TYLCSV.

67.(new) Method according to claim 66 wherein the viral gene sequence made an ineffective target of the virus-induced posttranscriptional gene silencing is the SEQ ID No 6 encoding for the capsid protein SEQ ID No 7.

68.(new) Method according to claim 55, wherein the plants, tissues or cells thereof belong to the group consisting of tomato, pepper, tobacco, squash, manioc, sweet potato, cotton, melon, potato, soybean, corn, wheat, sugar cane, bean, beet.